

ACGTTGACAC	AGGAATGAAG	AGTGTATTGG	CTGAATCTTC	AAGCAGAGGC	GATATTGACC	60
ATGTGCTTTT	TAAATTGGCC	TGCGTGACCC	GCCCACTTGG	TGTAAGAAGAA	GAACCGGCCA	120
AAGGGAGGGC	CTGAAGGACC	TCCACAGGAG	TGTGAGCAGC	ACTGCTTCAG	CAACAAAGCC	180
TCAGGTCCAC	ATCTTGGGAA	GAAT	ATG	GCC	ACT	231
			Met	Ala	Thr	
			1			
ATG	CTG	ATC	ATA	GCC	TGC	279
Met	Leu	Ile	Ile	Ala	Cys	
10					15	
CAG	ACC	TGG	TTT	GAA	GGT	327
Gln	Thr	Trp	Phe	Glu	Gly	
					30	
GTC	AGT	GCC	GGC	ACC	TTT	375
Val	Ser	Ala	Gly	Thr	Phe	
					45	
GGA	ACT	CGG	ATT	CAT	GTT	423
Gly	Thr	Arg	Ile	His	Val	
					60	
CTC	CCC	TTT	CTG	GAA	GGT	471
Leu	Pro	Phe	Leu	Glu	Gly	
					75	
TCT	GCT	TTT	GTG	GAT	CAG	519
Ser	Ala	Phe	Val	Asp	Gln	
					95	
CTC	TTG	GAG	GTG	GCC	AAA	567
Leu	Leu	Glu	Val	Ala	Lys	
					110	
ACC	CCG	GTG	GTT	CTG	AAA	615
Thr	Pro	Val	Val	Leu	Lys	
					125	
CAG	AAA	GCC	CAG	GCT	CTG	663
Gln	Lys	Ala	Gln	Ala	Leu	
					140	
TCA	CCT	TTC	CTG	GTC	CCA	711
Ser	Pro	Phe	Leu	Val	Pro	
					155	
TAT	GAA	GGC	ATA	CTA	GCC	759
Tyr	Glu	Gly	Ile	Leu	Ala	
					170	
CTG	CAT	GGT	CGT	GGC	CAG	807
Leu	His	Gly	Arg	Gly	Gln	
					190	
GCC	TCC	ACC	CAA	ATC	ACG	855
Ala	Ser	Thr	Gln	Ile	Thr	
					205	
CAA	ACA	CCT	AGG	GGC	TAC	903
Gln	Thr	Pro	Arg	Gly	Tyr	
					220	

FIG. 1

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTT Gly Lys Ala Trp Pro Glu Thr Arg Arg 460 465	1629

Fig. 1 (cont'd.)

TAGATGAGTC	TTGCTCTTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTTGCA	CATCTAATGT	1689
GAATAGCTCC	TAACCACTTG	GTGGGTGCAT	GGCTGGCACC	AGACTGTAAA	TCTTTTGGGA	1749
TTCTTTGTAC	AGAGTCCTGC	AAAGGAAAAA	AGAGAAAAGG	TTTGGAATC	CATGCTAGAT	1809
TGCGAGTTCA	GAGACAGGTC	CCTGGGGACC	AAAGAACAAT	CTCGTTTCAA	CCCTTGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTTC	TTATAAGCTG	ATTACTGAA	ATCCATAAC	1929
CCATCAATGC	TGTTAATTTT	TTTCTTCCTA	CCCTTATTAC	ATTCCCTACC	CTAAAAGCCT	1989
GGGGGAAATA	CCTGGTTTTG	CTTCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTATTAGAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATT	AAAGCTTAAA	2109
AAAAAAAAA						2119

Fig. 1 (cont'd.)

TUE 120 22 50000

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peaNTase 1 ----MELLKLTFFLTSPKXISSOYQONKLLTSRYFGKQSEIASVAVVFDAGSTGSR
potapyrase 1 RLNQNSHPFPIHLLPLVPLSLSSKNWNAQPLRRHLSHSE..HYAVVFDAGSTGSR
mNTase 1 KATSWGATPMHLLACGCTVFPYAGQQTWFGYPLSSHCPTNVSAQFVQINFDAGSTGSR
yGDPase 1 KTFKXILATPFENDEPGTLLQDSEKTSQNHPLADAKRSQTSQTCSEHRYVIMFDAGSTGSR

peaNTase 57 LHVYRFQDLDLLHIGKQVEYLYKLTPLGLSSYATFLOAANSILPLEQAEADVVPDLOP
potapyrase 59 VHVYRFDDKLLGLPICNNIEVFMAFEPGLSSYADPKAAANSILPLEQAEADVVPDLOP
mNTase 61 LHVYRFVORTAGOLFPEGSEIFDEKAPGLSATVQPKQCAETRGELLEAVDSIPRSHVE
yGDPase 61 VHVYRFEDVCTG..EPTLLDERFDMLEPGLSLEDTSVGAANSILPLEQAVANVYPIKARS

peaNTase 117 LTFVRLCATAGLRLLNGDASEKILQSVRDMLSNRSTF..NWQPDVMSINQTOEGSYLWVT
potapyrase 119 LTFPLRGATAGLRLLNGDANEKILQAVRNLYKNOSTF..HSKQDQVTHLQCTOEGSYWNAK
mNTase 121 LTFVRLKATAGLRLLPEKKAQALLLEVEENFRH..SPF..VVPDGSVSIHQSTEGILAHVT
yGDPase 119 CTFVANKATAGLRLLQDAKSSKILSAVRDMLERDTPFPVVGQGVSIHQSTEGVTFAMRT

peaNTase 176 VHYALGNLGRKRYTK..LVGVIDLGGGCVONHAYAVSKKTAKNAPKADGQDPVKKKVVTKG
potapyrase 178 LHYLLGNLGRDYSK..LTATIDLGGGCVONHAYALSNGQAKADQNEGC..RPVVOQKEHMS
mNTase 179 VHYLLGNLGRDYSK..LVGTIDLGGGCVONHAYALSNGQAKADQNEGC..RPVVOQKEHMS
yGDPase 179 LHYLLGNLGRDYSK..LVGTIDLGGGCVONHAYALSNGQAKADQNEGC..RPVVOQKEHMS

peaNTase 234 IPVCLVHVSYLEFGRFAGRAELRL.....DPRSPHPCGALFPHGIV
potapyrase 235 KHYCLVHVSYLEFGRFAGRAELRL.....DPRSPHPCGALFPHGIV
mNTase 232 STZKLYVHVSYLEFGRFAGRAELRL.....DPRSPHPCGALFPHGIV
yGDPase 234 EHYTLYVQPSHLCYCLERGRNKVNSVLVENALKDGKILKQDNTKPHULSPOCPFKVHTATN

peaNTase 276 TVSGCEPKATATTSQ.....NNAKQNTIRNALKKPHTPPYCNCTFGGHWNGCGGN...
potapyrase 277 TVSGCEPKATATTSQ.....NNAKQNTIRNALKKPHTPPYCNCTFGGHWNGCGGN...
mNTase 270 KCEFWLZARNIFQGV.....KYQYGGHGEQENGFEPCYAEVLRVVOGCDHQPEEVR...
yGDPase 294 EKYTLSEKHYTTIDFIFGDFEFGAQCEPFLTDEIKNKDAQCGSPFPGFNGVHQPSLVRFTK

peaNTase 328 GKNKTFASSSFHYLPEDTGHVDSTPNFYQNPVDIEIRAKEACALRFDAKSTFPLEKKE
potapyrase 329 GKNKTFASSSFHYLPEDTGHVDSTPNFYQNPVDIEIRAKEACALRFDAKSTFPLEKKE
mNTase 322 GSA..FYAPSYHYDRAADTHEIDYE..KQVLEVEDPERKAREVCH..HLQSFSSGSE.....
yGDPase 354 ESNGLYITFSYFYDRCPFLGHPLEPFLSENDLARIVCKGEDTMRREVREGHAGS...DDEL

peaNTase 388 HIASYVCHDLIYQVLLVDGFGCLPLQNLTHGNELEYOHATVLAAMPLOCAWYKATSLPR
potapyrase 389 HIASYVCHDLIYQVLLVDGFGCLPLQNLTHGNELEYOHATVLAAMPLOCAWYKATSLPR
mNTase 374 ...RLCHDLIYHITALLKGLGFAERPLAHRESQHRDWLGLQCHSPAPVSGHHQLR
yGDPase 411 ESDSHFCDLSGTVSLEHTGQDPLQQRHRAQHANKS...IQGCGASHPPLKKNQW

peaNTase 448 PERGMIFY-----
potapyrase 448 NRYASH-----
mNTase 430 FSTREAICISEPVFSQEGVDSETFSDLSGKAWPETR*
yGDPase 467 CKKQSA-----

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FIG. 2

[illegible]

**ACR II**

[illegible]

### ACR III

CD39	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553
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ACR IV

F16.3

GTGGGGTCGT	ATCCCGCGGG	TGGAGGCCGG	GGTGGCGCCG	GCCGGGGCGG	GGGAGCCCAA	60
AAGACCGGCT	GCCGCCTGCT	CCCCGGAAAA	GGGCACTCGT	CTCCGTGGGT	GTGGCGGAGC	120
GCGCGGTGCA	TGGAATGGGC	TATGTGAATG	AAAAAAGGTA	TCCGTTATGA	AACTTCCAGA	180
AAAACGAGCT	ACATTTTTC	GCAGCCGCAG	CACGGTCCTT	GGCAAACAAG	G ATG AGA	237
					Met Arg	
					1	
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC	285					
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro						
5 10 15						
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG	333					
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp						
20 25 30						
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC	381					
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala						
35 40 45 50						
CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429					
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala						
55 60 65						
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477					
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser						
70 75 80						
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA	525					
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu						
85 90 95						
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573					
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu						
100 105 110						
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621					
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu						
115 120 125 130						
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC	669					
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala						
135 140 145						
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717					
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly						
150 155 160						
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765					
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala						
165 170 175						
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813					
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr						
180 185 190						
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861					
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser						
195 200 205 210						
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909					
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly						
215 220 225						

FIG. 4

GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Ser Pro Cys Val Glu Gly Pro Ala Lys Asp Gly 275 280 285	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365 370	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445 450	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTGC ATAAACCCTC CTGTCCTGGA CGTGACTTCA TCCTGAGGAG CCACAGCACA GGCCGTGCTG GCACTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCCC TGGCATCAGC CTCTTCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC	1697 1757 1817

FIG. 4 (cont'd.)

AATGCCACCT	GTCTGCCTGG	GCTCCAAGTG	GGCAGGACCA	GGACAGAACC	ACAGGCACAC	1877
ACTGAGGGGG	CAGTGTGGCT	CCCTGCCTGT	CCCATCCCCA	TGCCCCGTCC	GCGGGGCTGT	1937
GGCTGCTGCT	GTGCATGTCC	CTGCGATGGG	AGTCTTGTCT	CCCAGCCTGT	CAGTTTCCTC	1997
CCCAGGGCAG	AGCTCCCCCT	CCTGCAAGAG	TCTGGGAGGC	GGTGCAGGCT	GTCCTGGCTG	2057
CTCTGGGGAA	GCCGAGGGAC	AGCCATAACA	CCCCCGGGAC	AGTAGGTCTG	GGCGGCACCA	2117
CTGGGGAATC	TGGACTTGAG	TGTGTTTGCT	CTTCCTTGGG	TATGAATGTG	TGAGTTCACC	2177
CAGAGGCCTG	CTCTCCTCAC	ACATTGTGTG	GTTTGGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAGGTGCC	CACCTTTCAG	GGAGTCTCCC	AGCATGGGCG	GATGCCGGGC	2297
ATGAGCTGCT	GTAAACTATT	TGTGGCTGTG	CTGCTTGAGT	GACGTCTCTG	TCGTGTGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACACC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGCTGTTCC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAG	CTCTCGGTGT	CTCGGGCCAC	2537
CATCCGCCCCA	CCTCGGGCTG	ACCCACCTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCCGTG	2597
CATCCTGCTC	AGTGTGGCGT	CAGTGTCTGG	GCTGAGCCCC	TTGAGCTGCT	TCAGTGAATG	2657
TACAGTGCCC	GGCACGAGCT	GAACCTCATG	TGTTCCACTC	CCAATAAAAG	GTTGACAGGG	2717
GCTTCTCCTT	CAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAA		2762

Fig. 4 (cont'd)

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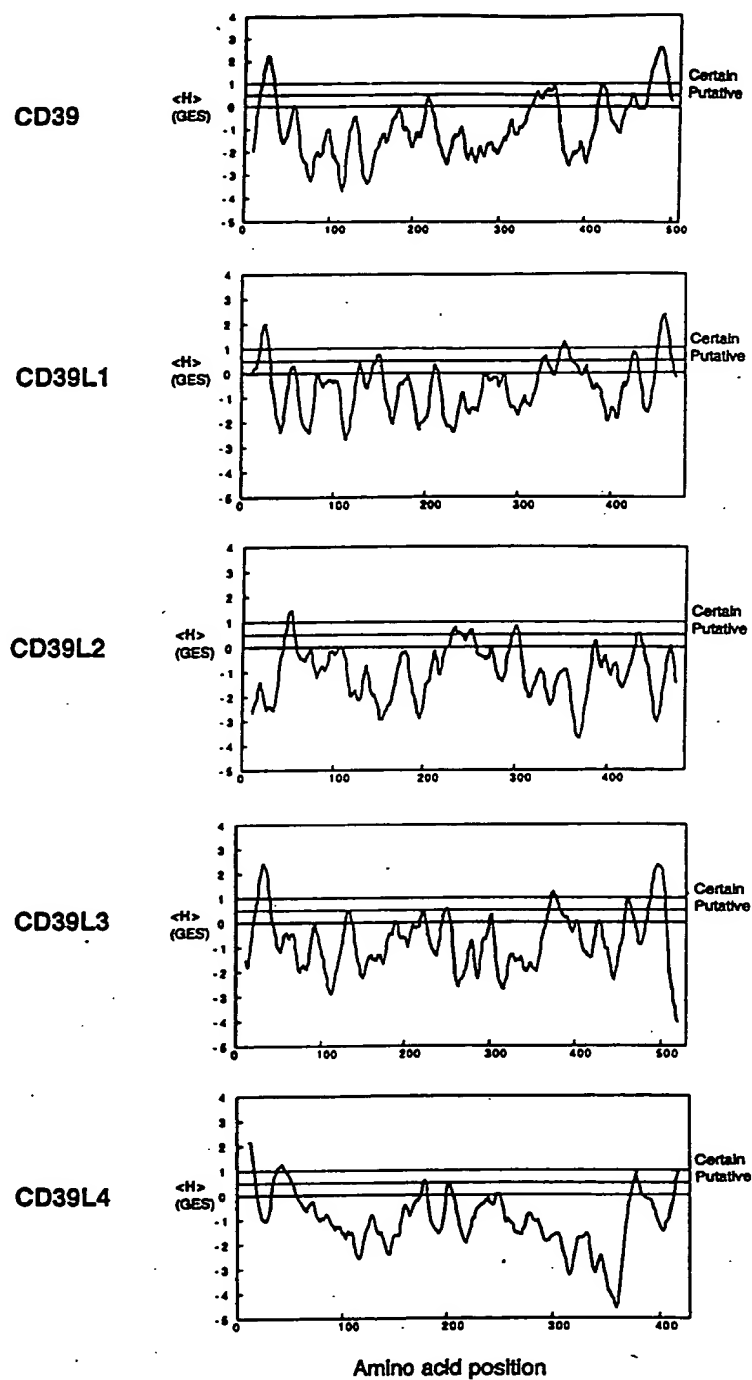


FIG. 5

ACCCACGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG	60
CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT	112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys	
1 5 10	
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC	160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala	
15 20 25	
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC	208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val	
30 35 40	
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT	256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly	
45 50 55	
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA	304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln	
60 65 70	
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Ser Gln Thr Phe	
75 80 85 90	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	
95 100 105	
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	
110 115 120	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	
125 130 135	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	
155 160 165 170	
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	

FIG. 6

ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr 235 240 245 250	832
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu 255 260 265	880
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Gln Asn Ser Pro Thr Lys 270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe 285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro 300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp 315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala 335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys 350 355 360	1168
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 365 370 375	1216
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 380 385 390	1264
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu 395 400 405 410	1312
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 415 420 425	1360
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440	1408
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455	1456
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu 460 465 470	1504
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr 475 480 485 490	1552

FIG. 6 (cont'd.)

CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA 1600  
 Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala  
 495 500 505

TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT 1648  
 Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe  
 510 515 520

GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC 1703  
 Asp His Ala Val Asp Ser Asp  
 525

TGCTTAGAGT CAGCCTGGGT GGCACCAGGC AATGCAGGTG AAGTGGCTGC CTTCAGGAAA 1763  
 TACAACCTAAC TAAATCAAA CACCTAGGTC ACGTGCCTCT CAAATACTGA TTTCTGCCAC 1823  
 AGCACCTCTT GAGGCATCCC TTGGCTATTC TGTGCATATT GTTCTTCAGA GACCTCACTA 1883  
 CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTC AGGCTCTTTA 1943  
 TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAATGT TGAAGAATTG 2003  
 ACCTCAGGGC TCAGTTTCCA TTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA 2063  
 AGCATTTTCG CAATCAGAAT CTCATTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT 2123  
 TTCTTGTAGC AATCTCGTAA GCAGTGAACC CCTCAGATC AGTAGAATAT AGTATCTGGG 2183  
 GGAGAAGACT TACTTCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA 2243  
 TCCCGAAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG 2303  
 GAATTCCCAC TTAGGGCTCT GGTCACCTAGA TTGCAACCTG TGTGTTTGTG ATCATCTCTCA 2363  
 TCTCACCATT GTATTGCTAT GCCCTCCCAT AAAAACACAT TGATCCCTAG CAAGATTATT 2423  
 GCATTCCAGA TTTTACTGCC TTGCTAGGC TTTTGCTTAG CAAAGGGCTG ACTTTCCATT 2483  
 GTTATCATGG TGTATATATT TTTGTACCA TTCCCACAAG TATACTTGAT GTTGTCTAG 2543  
 AACGAACATC CTACTCTATG ATTTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT 2603  
 GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTTATC 2663  
 TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAACTA AAAATCAGCA 2723  
 TTATTTTATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTTGA 2783  
 AAAAAAAAAA AAAA 2797

Fig. 6 (cont'd.)

GCGGCGCGCT	TTTCCTTGTT	CCTGGTCAAC	AAAGAAATGT	GGAGTGTCTT	GGCTGAATCC	60
TCATACAGAC	AAGATCATT	TGGTGCTGTT	AGGTAGGACT	TGTATCCAGA	TGTAAGGTTG	120
AAAAAGTGAT	ATAATAAAGG	AACCAAGGAG	AAAATTCAGA	AGGAAAGAAA	AAATTGCCTC	180
TGCAGGTGTG	CGAGCAGGAT	TGCTTCTGCA	ACAAAAGCCT	CCACCCAGCC	ACATCTTGGG	240
AAAAGA ATG	GCC ACT TCT	TGG GGC ACA	GTC TTT	TTC ATG CTG	GTG GTA	288
Met	Ala Thr Ser	Trp Gly Thr	Val Phe	Phe Met Leu	Val Val	
1		5		10		
TCC TGT GTT	TGC AGC GCT	GTC TCC CAC	AGG AAC CAG	CAG ACT TGG	TTT	336
Ser Cys Val	Cys Ser Ala	Val Ser His	Arg Asn Gln	Gln Gln Thr	Trp Phe	
15		20		25	30	
GAG GGT ATC	TTC CTG TCT	TCC ATG TGC	CCC ATC AAT	GTC AGC GCC	AGC	384
Glu Gly Ile	Phe Leu Ser	Ser Ser Met	Cys Pro Ile	Asn Val Ser	Ala Ser	
	35		40		45	
ACC TTG TAT	GGA ATT ATG	TTT GAT GCA	GGG AGC ACT	GGA ACT CGA	ATT	432
Thr Leu Tyr	Gly Ile Met	Phe Asp Ala	Gly Ser Thr	Gly Thr Arg	Ile	
	50		55		60	
CAT GTT TAC	ACC TTT GTG	CAG AAA ATG	CCA GGA CAG	CTT CCA ATT	CTA	480
His Val Tyr	Thr Phe Val	Gln Lys Met	Pro Gly Gln	Leu Pro Ile	Leu	
	65		70		75	
GAA GGG GAA	GTT TTT GAT	TCT GTG AAG	CCA GGA CTT	TCT GCT TTT	GTA	528
Glu Gly Glu	Val Phe Asp	Ser Val Lys	Pro Gly Leu	Ser Ala Phe	Val	
	80		85		90	
GAT CAA CCT	AAG CAG GGT	GCT GAG ACC	GTT CAA GGG	CTC TTA GAG	GTG	576
Asp Gln Pro	Lys Gln Ala	Glu Thr Val	Gln Gly Leu	Leu Leu Glu	Val	
	95		100		105	
GCC AAA GAC	TCA ATC CCC	CGA AGT CAC	TGG AAA AAG	ACC CCA GTG	GTC	624
Ala Lys Asp	Ser Ile Pro	Arg Ser His	Trp Lys Lys	Thr Pro Val	Val	
	115		120		125	
CTA AAG GCA	ACA GCA GGA	CTA CGC TTA	CTG CCA GAA	CAC AAA GCC	AAG	672
Leu Lys Ala	Thr Ala Gly	Leu Arg Leu	Leu Pro Glu	His Lys Ala	Lys	
	130		135		140	
GCT CTG CTC	TTT GAG GTA	AAG GAG ATC	TTC AGG AAG	TCA CCT TTC	CTG	720
Ala Leu Leu	Phe Glu Val	Lys Glu Ile	Phe Arg Lys	Ser Pro Phe	Leu	
	145		150		155	
GTA CCA AAG	GGC AGT GTT	AGC ATC ATG	GAT GGA TCC	GAC GAA GGC	ATA	768
Val Pro Lys	Gly Ser Val	Ser Ile Met	Asp Gly Ser	Asp Glu Gly	Ile	
	160		165		170	
TTA GCT TGG	GTT ACT GTG	AAT TTT CTG	ACA GGT CAG	CTG CAT GGC	CAC	816
Leu Ala Trp	Val Thr Val	Asn Phe Leu	Thr Gly Gln	Leu His Gly	His	
	175		180		185	
AGA CAG GAG	ACT GTG GGG	ACC TTG GAC	CTA GGG GGA	GCC TCC ACC	CAA	864
Arg Gln Glu	Thr Val Gly	Thr Leu Asp	Leu Gly Gly	Ala Ser Thr	Gln	
	195		200		205	
ATC ACG TTC	CTG CCC CAG	TTT GAG AAA	ACT CTG GAA	CAA ACT CCT	AGG	912
Ile Thr Phe	Leu Pro Gln	Phe Glu Lys	Thr Leu Glu	Gln Thr Pro	Arg	
	210		215		220	
GGC TAC CTC	ACT TCC TTT	GAG ATG TTT	AAC AGC ACT	TAT AAG CTC	TAT	960
Gly Tyr Leu	Thr Ser Phe	Glu Met Phe	Asn Ser Thr	Tyr Lys Leu	Tyr	
	225		230		235	

Fig. 7

ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr 240 245 250	1008
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser 255 260 265 270	1056
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val 275 280 285	1104
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro 290 295 300	1152
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro 305 310 315	1200
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp 320 325 330	1248
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu 335 340 345 350	1296
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu 355 360 365	1344
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr 370 375 380	1392
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val 385 390 395	1440
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu 400 405 410	1488
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His 415 420 425	1539
GTACTTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG TTTCTGAACT AGTCTGGGAC ATCCTGGACT TGAGCCTAGA GATTTAGGTT TAATTAATTT TACACATCTA ATGTGAACTG CTGCCTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTTGGAA CTTAACCTTG GAGTGAGAGC CCAGGGACAG GTCCCTGGAA ACCAAAGAAA AATCGCATT CAACCCTTTG AGTGCCTCAT TCCACTGAAT ATTTAAATTT TCCTCTTAAA TGGTAACTG ACTTATTGCA ATCCCAAGAC CCATCAATAT CAGTATTTTT TTCCTCCCTA TACAGTGCCC TGCCACCCCT TATCTGCACC CACCTCCCTT GAAAAAGAGA GAAAAAATAA AAAAAAATAA	1599 1659 1719 1779 1839 1899 1959 1998

FIG. 7 (cont'd.)

CD39L2 1 MKKGIRYETSAKTSYIFQOPQEGPMQTMRKISNHOGLRVAKVATPLGCVGVFVYVTR  
 CD39L4 1 -----  
 CD39L1 1 -----  
 CD39L3 1 -----  
 CD39 1 -----

## ACR I

CD39L2 61 NWEKATATOCFFSITRAAPTRNGQAESELGTAAGHEVYVCI DAGSGGVVYVTR  
 CD39L4 7 TVFFMLVVSCLSAFERNHOOTAFGLFSEMCPEVVSATLVCI DAGSGGVVYVTR  
 CD39L1 1 ---MAQKVEPLPFLNAAKALALLCVPTKVRPPKYGIVLDAGSSHTSRYVK  
 CD39L3 16 KATIRPFIILVYLLSIVLVSTIKOIKKVLPPKYGIVLDAGSSHTSRYVK  
 CD39 7 SNKATFCHNLDLITOFIIIVIALLAOLTONALPENVKYGIVLDAGSSHTSRYVK

## ACR II

CD39L2 120 FTAPPRPTPTTEAFKVRPGSAYADVIRKAOSELVAKODIDFDFKATPL  
 CD39L4 67 FVQKMPGQPLMKEGVDFSVHPCSATVDPRKAOSELVAKODIDFDFKATPL  
 CD39L1 58 NPAEKENDTGIVCDHSCDVPCQISVADNPSCAOSELVAKODIDFDFKATPL  
 CD39L3 75 NPAEKENDTGIVCDHSCDVPCQISVADNPSCAOSELVAKODIDFDFKATPL  
 CD39 67 NPAEKENDTGIVCDHSCDVPCQISVADNPSCAOSELVAKODIDFDFKATPL

## ACR II

## ACR III

CD39L2 178 VLKATAGRL...KQERAK...LKVKE...SPFLVODDCVSDIC...KQV...  
 CD39L4 126 VLKATAGRL...PEKAK...LKVKE...SPFLVODDCVSDIC...KQV...  
 CD39L1 114 VLKATAGRL...PEKAK...LKVKE...SPFLVODDCVSDIC...KQV...  
 CD39L3 135 VLKATAGRL...PEKAK...LKVKE...SPFLVODDCVSDIC...KQV...  
 CD39 127 VLKATAGRL...PEKAK...LKVKE...SPFLVODDCVSDIC...KQV...

## ACR IV

CD39L2 235 LKSSL...SPSCSVGMDLSCSTOIFLPRVETL...ASP...CYLTA...  
 CD39L4 183 LKSSL...SPSCSVGMDLSCSTOIFLPRVETL...ASP...CYLTA...  
 CD39L1 176 LKSSL...SPSCSVGMDLSCSTOIFLPRVETL...ASP...CYLTA...  
 CD39L3 193 LKSSL...SPSCSVGMDLSCSTOIFLPRVETL...ASP...CYLTA...  
 CD39 185 LKSSL...SPSCSVGMDLSCSTOIFLPRVETL...ASP...CYLTA...

CD39L2 283 MNTYKLYE...LGL...LGL...LGL...LGL...LGL...LGL...LGL...  
 CD39L4 231 MNTYKLYE...LGL...LGL...LGL...LGL...LGL...LGL...LGL...  
 CD39L1 229 MNTYKLYE...LGL...LGL...LGL...LGL...LGL...LGL...LGL...  
 CD39L3 248 MNTYKLYE...LGL...LGL...LGL...LGL...LGL...LGL...LGL...  
 CD39 242 MNTYKLYE...LGL...LGL...LGL...LGL...LGL...LGL...LGL...

CD39L2 343 VSG...KAAAS...EEL...AAR...FSEV...QTR...HRE...EV...  
 CD39L4 290 VSG...KAAAS...EEL...AAR...FSEV...QTR...HRE...EV...  
 CD39L1 283 VSG...KAAAS...EEL...AAR...FSEV...QTR...HRE...EV...  
 CD39L3 307 VSG...KAAAS...EEL...AAR...FSEV...QTR...HRE...EV...  
 CD39 300 VSG...KAAAS...EEL...AAR...FSEV...QTR...HRE...EV...

CD39L2 403 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...  
 CD39L4 350 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...  
 CD39L1 342 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...  
 CD39L3 367 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...  
 CD39 357 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...

CD39L2 462 LSWALGANPH...D...L...K...S...  
 CD39L4 410 LSWALGANPH...D...L...K...S...  
 CD39L1 384 LSWALGANPH...D...L...K...S...  
 CD39L3 418 LSWALGANPH...D...L...K...S...  
 CD39 409 LSWALGANPH...D...L...K...S...

CD39L2 485 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...  
 CD39L4 429 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...  
 CD39L1 432 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...  
 CD39L3 478 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...  
 CD39 468 LKVGOPH...KAYVC...LST...OPSS...PFS...L...L...L...

FIG. 8

[illegible]

```

peaGDP      1  -----
potapyrase  1  -----
CD39L2      1  MKKGIRYKTSRKTSYIFQOPQHGPQTIRKLNHGSLRLVIVTFLGLCVGVYIYKHN
CD39L4      1  -----
dATPase     1  -----
yGDPase     1  -----

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```

peaGDP      2 K LKLLITPFEFSPIILSYLLNHHLLTSRKIFREBISSYAFDAGTSGSRHVV
potaprase   6 SEPIITLFLVLDFLSTHNAVYILPRLHLLHSELYAFDAGTSGSRVHVH
cd39L2      61 KWEKATATQAFSSTRFGARWGQAHKSPFLAAQCHEVYIIFDAGTSGRVHV
cd39L4      7 TFFHVEVCVCSAVRRKQTHQHLSSCFHVSASTLYIIFDAGTSGRVHV
dntPase     37 KISYLCILIVNILLFVTVGVSEHASPRLRLSKFYSLQVVALFDAGTSGSRVLA
yGDPase     5 DSIILPNDKPGTQDSKIKQRYPLADAKSQSQTCSEHRYVILFDAGTSGSRVH-Y

```

**ACR II**

```
peaGDP      61  F N O M L D L L E I S K G E Y K G P C L S S Y A P E Q A A N S L P L L Q A D V V P D L Q K T P V
potatypase  63  E K K L G L G L I S E E Y E M A T E P C L S S Y A D P K A A N S L P L L D G A G V V R L O S E T P V
CD39L4      119 Q T T P P R E T P T E D E K A V K P G L S Y A D D V E A A G R E L L I D V N O D P F Q F K A T P V
CD39L2      66  T V Q K P Q O L P L P T C E D V D V K P G L S Y D D P Q A E G L L V A K D S P E E K K T P V
dHTPase     96  K E R S R D T D M K L V T E D K I R K P G L S S D P A A H S K L L L D A A T P E N S G S T P V
yODPase     65  K E I . . . C T S P L L D E A D M P G L S S D D P S V A A H S L P L L V A A T V E T T A S C T P V
```



		ACR II	ACR III
peaGRP	121	REKATAGRLRLGGDAERIKLOVVRDLSENSTF	EVVQDAVSI DGTGGSTLVTVNYA
potapyrase	123	ELCATAGRLRLGGDAEKILQAVRDLSENSTF	EGKQDQVVI DGTGCGSTLVTNYE
CD39L2	178	VLKATAGRLRLFGKAKKLOKVVTFKASPF	EVQGDGVSIK CGDCEGSAITNYL
CD39L4	126	VLKATAGRLRLPERRAKALFFLVVTFKASPF	EVQGDGVSIKCG DCG LKAVTVNL
dHTase	156	VLKATAGRLRLP KAEKILAVRDLFAKSES	EVVQDAVSIKIGTDCG LKAVTVNL
YDPase	123	AKATAGRLRLGGDAERIKLSAVRDLKDYPTF	EVQGDGVSIKCG EGVAKAVTNYL

ACR IV

```
peaGDP      180  LGHLGKRYTK...TVGV  DLGGGSV  AAVS  KITAKAPVADGD  PY  KIVVEKQIPV
potatypase  182  LGHLGRDMYTK...TGV  DLGGGSV  AAVS  EQFAKAPONEDG  PY  QKHKMSKIDVN
CD139L2     236  TGHKTFPGG...  FVGL  LDLGGSTCI  AAF  FVEG  ....T  IASFPGLTAR  RST  TYK
CD139L4     184  TGLDPCRHR...  FVGL  LDLGGSTCI  AAF  FVEG  ....T  ETPTGKLTSE  GNSYTK
yGTPase     214  GRLSNTG...  A...  DLGGGSV  ST  F  FDF  ....DVPYTK  LER  VVTSKKIKIN
4DTPase     183  CGHCGAKPL...  FVGL  DLGGGSV  ST  F  FPIPKV  NV  ....DGRIK  VKTCHENV
```

```

peaGDP      238  LYTHSYLMEFGRLAARAEILNLTPGG.....MFCLLAGFNG...
potapylase  239  LYTHSYLNLGQALAARAEILNLRMS...MFCLNLECGCR...
CD19L2      289  LYTHSYLGLGLARLAIDQLGQEGPDKGKLV...SPCLSPSFGC...
CD19L4      237  LYTHSYLGLGLARLAATLQALELTCGCTT...SACLPRWLL...
dNTPase     264  LYTHSYLGLGLARAEAF...TCGKKTDTLL...SVCMPPIAH...
yGDPase     238  LYQPSHLGGLIKETREKAGVLVZALKDGKLLGDMTKTHQLSPCLPPKVNTHKKT

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peaGDP      276  TYEGEE KA ITTG EEFKCHTIR ALKLTIPSPYQHCTFGG WHGG...SGMGQKN
potapylase  277  YGCVGVYKVK PEGS SSWKRCRTRRLALK HANCA EECTFNGVWHGG...SGDGQKN
CD39L2     335  EHLEVTYVSG K ASLLELCAR...SE...QNAV...ERT...EVKVEV
CD39L4     282  ILGGVKKYQCG QEGEVSSEECIN...VL...VRGKL...KQF...EVVQVS
dntPase    308  PYGMVYKVKSGKEKSSAQQPIVDFDCLL...KSKVMPLKPKP...FTKQRA
XTPase     298  LESKTYTIDPQIDPSQACRITLDEHEK ACGSPPCSHNGVPSLVATFKKSL

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```

peaGDP      332  EAGSSSF1YLPE2DTCHGVDA3TP4NT5LT6VP7DIETRAKEACAL8IFEDAKS9CPPFLDK10NT11S
potapylase  333  IEAGS1:FYD2LAAGV3:VD4K5PS6LARPI7DLAAHVAC8QTV9DIKSI10PKK11Q12NI13F14
CD39L2     379  FYAFSG1YDLAAGV2:DAE3:LGGGLV4GD5EIAK6IVCRT7.....LEA8FP9SSP10
CD39L4     326  FYAFSY1YDRAV2QTD3DAE4:LGGILK5VED6:E7KAE8VECDN9.....LEA10FTSGSP11
dHTPase    360  LAFSY1.....RAIS2SG3VDPL4ASGETTV5ED6NKAG7ICAI8.....PMDE9.....CP10
YDPase     358  FYI1SYFYDR2LRPL3GMPL4FLNLE5VD6DA7IVCK8BE9WNV10EN11CHAGL12.....DELESD13

```

```

peaGDP      392  ECHDLIIYQIVLLVDGFGFLPCKRTSSKRIITQARVEAAWFLGAEVEASLSPKFERM
potapylase  392  ECHDLIDIYVLLVDGFGFLPCKRIITDQYKIVQCAAEVLGCAIDLSSTNKKIRM
CD39L2     428  FCHCDLTVVLLDGLGFGFSPKRVKLTAKDN...VEEVALGAEPHYDSNHEGFP
CD39L4     378  FLCHCDLTVVLLDGLGFGFADSTVQKLTAKDN...VEEVALGAEPHILDSIGIS--
dntPase    406  ETCFDLTVLSTLLRCFGLGDCCKRIKTKRIDG...REVEALGAEPHILSDPKFNS
yGDPase    415  ETCFDLTVVLLDGLGFGFSPKRVKLTAKDN...VEEVALGAEPLPKLSDHWKIRM

```

peaGDP	452	MYFV
potapyrase	452	SS:*
CD39L2	483	SS:-
CD39L4	429	----
dHTPase	462	----
GDPase	471	QS:-

FIG. 9